



SEQUENCE LISTING

<110> Glotzer, Michael  
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<120> Cyk-4 polypeptides, DNA molecules encoding them and their use in  
screening methods

<130> 0652.2260001/EKS/AES

<140> US 09/881,736

<141> 2001-06-18

<150> EP 00 112 880.0

<151> 2000-06-19

<150> EP 01 110 554.1

<151> 2001-04-30

<150> 60/241,231

<151> 2000-10-18

<150> To be determined

<151> 2001-06-13

<160> 8

<170> PatentIn Ver. 2.1

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<211> 3050

<212> DNA

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<221> 3'UTR

<222> (1970)..(3050)

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Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu

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Gly	Pro	Pro	Gly	Pro	Val	Lys	Lys	Thr	Arg	Ser	Ile	Gly	Ser	Ala	Val	195	200	205	
Asp	Gln	Gly	Asn	Glu	Ser	Ile	Val	Ala	Lys	Thr	Thr	Val	Thr	Val	Pro	210	215	220	
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Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp						
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Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile						
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Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe						
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Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro						
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Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile						
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Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu						
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Leu	Met	Ile	His	Leu	Gln	Arg	Val	Ser	Gln	Ser	Pro	Asp	Thr	Lys	Met	
			480					485					490			
gat	att	gcc	aat	cta	gct	aaa	gtc	ttt	ggc	cct	aca	ata	gtt	gcc	cat	1658
Asp	Ile	Ala	Asn	Leu	Ala	Lys	Val	Phe	Gly	Pro	Thr	Ile	Val	Ala	His	
		495					500					505				
act	gtg	ccc	aat	cca	gat	cca	gtg	aca	atg	ttc	cag	gac	atc	aaa	cgt	1706
Thr	Val	Pro	Asn	Pro	Asp	Pro	Val	Thr	Met	Phe	Gln	Asp	Ile	Lys	Arg	
	510					515					520					
cag	ctc	aag	gtg	gtg	gag	cgc	cta	ctc	tct	ctc	ccc	ttg	gag	tac	tgg	1754
Gln	Leu	Lys	Val	Val	Glu	Arg	Leu	Leu	Ser	Leu	Pro	Leu	Glu	Tyr	Trp	
525					530					535					540	
aat	cag	ttc	atg	atg	gtg	gac	caa	gag	aac	ata	gac	agc	cag	cga	ggc	1802
Asn	Gln	Phe	Met	Met	Val	Asp	Gln	Glu	Asn	Ile	Asp	Ser	Gln	Arg	Gly	
				545					550					555		
aat	gga	aac	tca	aca	cca	cgc	aca	cca	gac	gtt	aaa	gtg	agc	tta	ctg	1850
Asn	Gly	Asn	Ser	Thr	Pro	Arg	Thr	Pro	Asp	Val	Lys	Val	Ser	Leu	Leu	

560	565	570	
ggg cct gtg acc act cct gaa ttc cag ctt gtc aag act cct tta tca			1898
Gly Pro Val Thr Thr Pro Glu Phe Gln Leu Val Lys Thr Pro Leu Ser			
575	580	585	
agt tcc ctg tca cag agg ttg tac aac ctc tcc aag agc aca ccc aga			1946
Ser Ser Leu Ser Gln Arg Leu Tyr Asn Leu Ser Lys Ser Thr Pro Arg			
590	595	600	
ttt ggg aac aag agc aag tct gcc acc aac tta ggt caa cag ggc aaa			1994
Phe Gly Asn Lys Ser Lys Ser Ala Thr Asn Leu Gly Gln Gln Gly Lys			
605	610	615	620
ttt ttc cct gct ccg tac ctc aag taa agctgtgtct gcctgtgttt			2041
Phe Phe Pro Ala Pro Tyr Leu Lys			
625			
actgcacgag acacccctgt ctgctcttca gcctcctgtg taatgactac ttttagcatt			2101
ttccagactt taaataaagt tgaacgcgta tgagagtttg agtgttgcat agtccctcc			2161
cacctggaca cttagcacct ttactagttg tcgggagctt taaaatagga gatctttacc			2221
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tttggttaa agccaaatac tgctcatgaa atgactttgc tgtggtgtca cttagacaat			2341
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gcagcggccc cttctcagaa cacaggcctc ttcctccttc ggggactgac aagaagcttg			2461
gagccctcag cgggatgggc cgggccactg atctgaggat gcttcacttc tgtctgggtt			2521
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ccctgggatg ttttctgacc catactaacc cttacctgta acatgtatct ggaatattat			2881
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&lt;210&gt; 4

&lt;211&gt; 628

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 4

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Arg	Arg	Met	Glu	Ile	Ile	Asn	Glu	Gly	Asn	Glu	Ser	Ile	Glu	Phe	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Gln	Val	Val	Lys	Asp	Phe	Glu	Asp	Phe	Arg	Lys	Lys	Tyr	Gln	Arg	Thr
		35					40					45			
Asn	Gln	Glu	Leu	Glu	Lys	Phe	Lys	Asp	Leu	Leu	Leu	Lys	Ala	Glu	Thr
	50					55					60				
Gly	Arg	Ser	Ala	Leu	Asp	Val	Lys	Leu	Lys	His	Ala	Arg	Asn	Gln	Val
65					70					75					80
Asp	Val	Glu	Ile	Lys	Arg	Arg	Gln	Arg	Ala	Glu	Ala	Glu	Cys	Ala	Lys
				85					90					95	
Leu	Glu	Gln	Gln	Ile	Gln	Leu	Ile	Arg	Asp	Ile	Leu	Met	Cys	Asp	Thr
			100					105					110		
Ser	Gly	Ser	Ile	Gln	Leu	Ser	Glu	Glu	Gln	Lys	Ser	Ala	Leu	Ala	Phe
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Leu	Asn	Arg	Gly	Gln	Ala	Ser	Ser	Gly	His	Ala	Gly	Asn	Asn	Arg	Leu
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Ser	Thr	Ile	Asp	Glu	Ser	Gly	Ser	Ile	Leu	Ser	Asp	Ile	Ser	Phe	Asp
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Lys	Thr	Asp	Glu	Ser	Leu	Asp	Trp	Asp	Ser	Ser	Leu	Val	Lys	Asn	Phe
				165				170						175	
Lys	Met	Lys	Lys	Arg	Glu	Lys	Arg	Arg	Ser	Asn	Ser	Arg	Gln	Phe	Ile
			180					185					190		
Asp	Gly	Pro	Pro	Gly	Pro	Val	Lys	Lys	Thr	Cys	Ser	Ile	Gly	Ser	Thr
		195					200					205			
Val	Asp	Gln	Ala	Asn	Glu	Ser	Ile	Val	Ala	Lys	Thr	Thr	Val	Thr	Val
	210					215					220				
Pro	Ser	Asp	Gly	Gly	Pro	Ile	Glu	Ala	Val	Ser	Thr	Ile	Glu	Thr	Leu
225					230					235					240
Pro	Ser	Trp	Thr	Arg	Ser	Arg	Gly	Lys	Ser	Gly	Pro	Leu	Gln	Pro	Val
				245					250					255	
Asn	Ser	Asp	Ser	Ala	Leu	Asn	Ser	Arg	Pro	Leu	Glu	Pro	Arg	Thr	Asp
			260					265					270		
Thr	Asp	Asn	Leu	Gly	Thr	Pro	Gln	Asn	Thr	Gly	Gly	Met	Arg	Leu	His
		275					280					285			
Asp	Phe	Val	Ser	Lys	Thr	Val	Ile	Lys	Pro	Glu	Ser	Cys	Val	Pro	Cys
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Gly	Lys	Arg	Ile	Lys	Phe	Gly	Lys	Leu	Ser	Leu	Lys	Cys	Arg	Asp	Cys
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Arg	Leu	Val	Ser	His	Pro	Glu	Cys	Arg	Asp	Arg	Cys	Pro	Leu	Pro	Cys
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Ile	Pro	Pro	Leu	Val	Gly	Thr	Pro	Val	Lys	Ile	Gly	Glu	Gly	Met	Leu

340					345					350					
Ala	Asp	Phe	Val	Ser	Gln	Ala	Ser	Pro	Met	Ile	Pro	Ala	Ile	Val	Val
		355					360					365			
Ser	Cys	Val	Asn	Glu	Ile	Glu	Gln	Arg	Gly	Leu	Thr	Glu	Ala	Gly	Leu
	370					375					380				
Tyr	Arg	Ile	Ser	Gly	Cys	Asp	Arg	Thr	Val	Lys	Glu	Leu	Lys	Glu	Lys
385						390					395				400
Phe	Leu	Lys	Val	Lys	Thr	Val	Pro	Leu	Leu	Ser	Lys	Val	Asp	Asp	Ile
				405					410					415	
His	Val	Ile	Cys	Ser	Leu	Leu	Lys	Asp	Phe	Leu	Arg	Asn	Leu	Lys	Glu
			420					425					430		
Pro	Leu	Leu	Thr	Phe	Trp	Leu	Ser	Lys	Ala	Phe	Met	Glu	Ala	Ala	Glu
			435				440					445			
Ile	Thr	Asp	Glu	Asp	Asn	Ser	Thr	Ala	Ala	Met	Tyr	Gln	Ala	Val	Ser
	450					455					460				
Glu	Leu	Pro	Gln	Ala	Asn	Arg	Asp	Thr	Leu	Ala	Phe	Leu	Met	Ile	His
465						470					475				480
Leu	Gln	Arg	Val	Ser	Gln	Ser	Pro	Asp	Thr	Lys	Met	Asp	Ile	Ala	Asn
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Leu	Ala	Lys	Val	Phe	Gly	Pro	Thr	Ile	Val	Ala	His	Thr	Val	Pro	Asn
			500					505					510		
Pro	Asp	Pro	Val	Thr	Met	Phe	Gln	Asp	Ile	Lys	Arg	Gln	Leu	Lys	Val
		515					520					525			
Val	Glu	Arg	Leu	Leu	Ser	Leu	Pro	Leu	Glu	Tyr	Trp	Asn	Gln	Phe	Met
	530					535					540				
Met	Val	Asp	Gln	Glu	Asn	Ile	Asp	Ser	Gln	Arg	Gly	Asn	Gly	Asn	Ser
545						550					555				560
Thr	Pro	Arg	Thr	Pro	Asp	Val	Lys	Val	Ser	Leu	Leu	Gly	Pro	Val	Thr
				565					570					575	
Thr	Pro	Glu	Phe	Gln	Leu	Val	Lys	Thr	Pro	Leu	Ser	Ser	Ser	Leu	Ser
			580					585					590		
Gln	Arg	Leu	Tyr	Asn	Leu	Ser	Lys	Ser	Thr	Pro	Arg	Phe	Gly	Asn	Lys
		595					600					605			
Ser	Lys	Ser	Ala	Thr	Asn	Leu	Gly	Gln	Gln	Gly	Lys	Phe	Phe	Pro	Ala
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Pro	Tyr	Leu	Lys												
625															

&lt;210&gt; 5

&lt;211&gt; 2046

&lt;212&gt; DNA

<213> *Caenorhabditis elegans*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2046)

&lt;400&gt; 5

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cac att ttc aac atg att cta aac tca cag cga ccg caa ttc gat att	96
His Ile Phe Asn Met Ile Leu Asn Ser Gln Arg Pro Gln Phe Asp Ile	
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aag gat ata gga atg ttt cat ttg att gat gag att gag cgt ctc cgc	144
Lys Asp Ile Gly Met Phe His Leu Ile Asp Glu Ile Glu Arg Leu Arg	
35 40 45	
aag ctg tgg aaa gat tcc gag gaa tcc aaa aag cgg ctg aat gca gat	192
Lys Leu Trp Lys Asp Ser Glu Glu Ser Lys Lys Arg Leu Asn Ala Asp	
50 55 60	
atg aga gag gcc gaa gaa gca ctt gca aaa gct cgc aag aag ctg gca	240
Met Arg Glu Ala Glu Glu Ala Leu Ala Lys Ala Arg Lys Lys Leu Ala	
65 70 75 80	
atg ttc gat atc gat gtc aaa gac act cag aaa cat tta cgc gcg ttg	288
Met Phe Asp Ile Asp Val Lys Asp Thr Gln Lys His Leu Arg Ala Leu	
85 90 95	
atg gaa gaa aat aag gcg ttg aag ctc gat cta aac gtc tac gag act	336
Met Glu Glu Asn Lys Ala Leu Lys Leu Asp Leu Asn Val Tyr Glu Thr	
100 105 110	
cgt gaa aag cag ctg aaa gat gcg atg aag aac ggt ata ttc aat agt	384
Arg Glu Lys Gln Leu Lys Asp Ala Met Lys Asn Gly Ile Phe Asn Ser	
115 120 125	
ctc acc aag gaa gac cgc gat cag ttc aag ttt ctt cac gag cca ctg	432
Leu Thr Lys Glu Asp Arg Asp Gln Phe Lys Phe Leu His Glu Pro Leu	
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gtc cgg aca tac tcg aaa cgg gtg cag cag agg cat cca cat ttg atg	480
Val Arg Thr Tyr Ser Lys Arg Val Gln Gln Arg His Pro His Leu Met	
145 150 155 160	
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Glu Asp Thr Gln Asp Asp Glu Asp Asp Ser Glu Val Asp Tyr Asp Glu	
165 170 175	
act gga gac agt ttc gag gaa gtt att cat ttg cgc aat gga aga gag	576
Thr Gly Asp Ser Phe Glu Glu Val Ile His Leu Arg Asn Gly Arg Glu	
180 185 190	
gtc aga aga agc tca gct gct gga aac gca gtt ggt ggc aag cgg aga	624
Val Arg Arg Ser Ser Ala Ala Gly Asn Ala Val Gly Gly Lys Arg Arg	
195 200 205	

agc gcg tca gca cat gcg att act gct gct gcc aat tcg aag agg agc	672
Ser Ala Ser Ala His Ala Ile Thr Ala Ala Ala Asn Ser Lys Arg Ser	
210 215 220	
aga agc cgt gtt atg aca gct act ata gat gaa gag ccg aat gag ggt	720
Arg Ser Arg Val Met Thr Ala Thr Ile Asp Glu Glu Pro Asn Glu Gly	
225 230 235 240	
ggt aca cct cca aaa aga tgc cgt gat gat ggt tct aca cct cat caa	768
Gly Thr Pro Pro Lys Arg Cys Arg Asp Asp Gly Ser Thr Pro His Gln	
245 250 255	
gaa atg aca act acc acc act acc acc acc act act att cat aac	816
Glu Met Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile His Asn	
260 265 270	
tct cga gct cag aac cag gac ccg cca cgt gtc tca ctt cac cgc cag	864
Ser Arg Ala Gln Asn Gln Asp Pro Pro Arg Val Ser Leu His Arg Gln	
275 280 285	
ctc acc cgc agg agc ttg agc tgt gga agt att cca tca tgc gat caa	912
Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln	
290 295 300	
aca cca gga caa acc aca aat aac atc ggc ctc ggc atg tcg tcc gcc	960
Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala	
305 310 315 320	
att ctc acc aaa agc aca ctt gat atc cga acc ctg aaa cgt ggc acg	1008
Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr	
325 330 335	
ccg gcg tgg act aat gga aca act cgt gac atc gca atg aga cca cac	1056
Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His	
340 345 350	
acg ttt ata gag gca gga atc aaa gcg atg cga aaa tgc gac aaa tgt	1104
Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys	
355 360 365	
gct aca gcc ctg aag ctc gcc aca tca atg aaa tgc aga gac tgt cac	1152
Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His	
370 375 380	
cag gtt gtc cat cgt agt tgc tgc aac aaa ctt cat ctc ccg tgc ata	1200
Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile	
385 390 395 400	
cca cgc ccc aag acg atg atg acg ccg aaa tcc gca tta cgt gga gcc	1248
Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala	
405 410 415	
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Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala	
420 425 430	
aag cca atg atc ccg gca gca gtt att cat tgt gtg gtt gcc ctg gag	1344
Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu	
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 <213> *Caenorhabditis elegans*

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			20					25					30				
Lys	Asp	Ile	Gly	Met	Phe	His	Leu	Ile	Asp	Glu	Ile	Glu	Arg	Leu	Arg		
		35					40					45					
Lys	Leu	Trp	Lys	Asp	Ser	Glu	Glu	Ser	Lys	Lys	Arg	Leu	Asn	Ala	Asp		
	50					55					60						
Met	Arg	Glu	Ala	Glu	Glu	Ala	Leu	Ala	Lys	Ala	Arg	Lys	Lys	Leu	Ala		
65					70					75					80		
Met	Phe	Asp	Ile	Asp	Val	Lys	Asp	Thr	Gln	Lys	His	Leu	Arg	Ala	Leu		
				85					90						95		
Met	Glu	Glu	Asn	Lys	Ala	Leu	Lys	Leu	Asp	Leu	Asn	Val	Tyr	Glu	Thr		
			100					105					110				
Arg	Glu	Lys	Gln	Leu	Lys	Asp	Ala	Met	Lys	Asn	Gly	Ile	Phe	Asn	Ser		
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Leu	Thr	Lys	Glu	Asp	Arg	Asp	Gln	Phe	Lys	Phe	Leu	His	Glu	Pro	Leu		
	130					135					140						
Val	Arg	Thr	Tyr	Ser	Lys	Arg	Val	Gln	Gln	Arg	His	Pro	His	Leu	Met		
145					150					155					160		
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				165				170						175			
Thr	Gly	Asp	Ser	Phe	Glu	Glu	Val	Ile	His	Leu	Arg	Asn	Gly	Arg	Glu		
			180					185					190				
Val	Arg	Arg	Ser	Ser	Ala	Ala	Gly	Asn	Ala	Val	Gly	Gly	Lys	Arg	Arg		
		195					200					205					
Ser	Ala	Ser	Ala	His	Ala	Ile	Thr	Ala	Ala	Ala	Asn	Ser	Lys	Arg	Ser		
	210					215					220						
Arg	Ser	Arg	Val	Met	Thr	Ala	Thr	Ile	Asp	Glu	Glu	Pro	Asn	Glu	Gly		
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Gly	Thr	Pro	Pro	Lys	Arg	Cys	Arg	Asp	Asp	Gly	Ser	Thr	Pro	His	Gln		
				245					250					255			
Glu	Met	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ile	His	Asn		
			260					265					270				
Ser	Arg	Ala	Gln	Asn	Gln	Asp	Pro	Pro	Arg	Val	Ser	Leu	His	Arg	Gln		
		275					280					285					



Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln  
 290 295 300  
 Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala  
 305 310 315 320  
 Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr  
 325 330 335  
 Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His  
 340 345 350  
 Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys  
 355 360 365  
 Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His  
 370 375 380  
 Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile  
 385 390 395 400  
 Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala  
 405 410 415  
 Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala  
 420 425 430  
 Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu  
 435 440 445  
 Ala Arg Gly Leu Thr Gln Glu Gly Ile Tyr Arg Val Pro Gly Gln Val  
 450 455 460  
 Arg Thr Val Asn Val Leu Leu Asp Glu Leu Arg Ser Lys Thr Val Pro  
 465 470 475 480  
 Asn Val Gly Leu His Asp Val Glu Val Ile Thr Asp Thr Leu Lys Arg  
 485 490 495  
 Phe Leu Arg Asp Leu Lys Asp Pro Leu Ile Pro Arg Thr Ser Arg Gln  
 500 505 510  
 Glu Leu Ile Val Ala Ala Asn Leu Tyr Ser Thr Asp Pro Asp Asn Gly  
 515 520 525  
 Arg Leu Ala Leu Asn Arg Val Ile Cys Glu Leu Pro Gln Ala Asn Arg  
 530 535 540  
 Asp Thr Leu Ala Tyr Leu Phe Ile His Trp Arg Lys Val Ile Ala Gln  
 545 550 555 560  
 Ser Ser Arg Asn Lys Met Asn Cys Glu Ala Met Ala Arg Met Val Ala  
 565 570 575  
 Pro Ala Val Met Gly His Pro Val Lys Gln Ser Gln Ser Gln Ala Ile  
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 Ala Gly Arg Asp Ala Thr Asp Cys His Arg Ala Met Thr Ala Leu Phe  
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 Glu Phe Asp Asp Val Tyr Trp Gln Arg Phe Leu Gly Thr Ser Ala Val

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                     645                      650                      655  
  
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 Arg Leu Cys Pro Tyr Thr Gly Ser Thr Pro Ser Leu Ile Ala Ile Asp  
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 Glu Gly Ser Ile Gln Thr Val Leu Pro Pro Ala Gln Phe Arg Arg Glu  
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 Asn Ala Pro Gln Val Glu Lys Val Phe Arg Phe Gly Arg Val Phe Ser  
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 Glu Asn Asp Gly Gln Ala Thr Val Phe Glu Arg Thr Ser Val Asp Leu  
                     85                      90                      95  
  
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                     100                      105                      110  
  
 Val Thr Gly Ser Gly Lys Thr Tyr Thr Met Thr Gly Lys Pro Thr Glu  
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 Thr Gly Thr Gly Leu Leu Pro Arg Thr Leu Asp Val Ile Phe Asn Ser  
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 Ile Asn Asn Arg Val Glu Lys Cys Ile Phe Tyr Pro Ser Ala Leu Asn  
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Thr	Phe	Glu	Ile	Arg	Ala	Thr	Leu	Asp	Ala	His	Leu	Lys	Arg	His	Gln
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Met	Ala	Ala	Asp	Arg	Leu	Ser	Thr	Ser	Arg	Glu	Ile	Thr	Asp	Arg	Tyr
			180					185					190		
Cys	Glu	Ala	Ile	Lys	Leu	Ser	Gly	Tyr	Asn	Asp	Asp	Met	Val	Cys	Ser
		195					200					205			
Val	Phe	Val	Thr	Tyr	Val	Glu	Ile	Tyr	Asn	Asn	Tyr	Cys	Tyr	Asp	Leu
	210					215					220				
Leu	Glu	Asp	Ala	Arg	Asn	Gly	Val	Leu	Thr	Lys	Arg	Glu	Ile	Arg	His
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Asp	Arg	Gln	Gln	Gln	Met	Tyr	Val	Asp	Gly	Ala	Lys	Asp	Val	Glu	Val
				245					250					255	
Ser	Ser	Ser	Glu	Glu	Ala	Leu	Glu	Val	Phe	Cys	Leu	Gly	Glu	Glu	Arg
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Arg	Arg	Val	Ser	Ser	Thr	Leu	Leu	Asn	Lys	Asp	Ser	Ser	Arg	Ser	His
		275					280					285			
Ser	Val	Phe	Thr	Ile	Lys	Leu	Val	Met	Ala	Pro	Arg	Ala	Tyr	Glu	Thr
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Lys	Ser	Val	Tyr	Pro	Thr	Met	Asp	Ser	Ser	Gln	Ile	Ile	Val	Ser	Gln
305					310					315					320
Leu	Cys	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Ala	Lys	Arg	Thr	Gln
				325					330					335	
Asn	Val	Gly	Glu	Arg	Leu	Ala	Glu	Ala	Asn	Ser	Ile	Asn	Gln	Ser	Leu
			340					345					350		
Met	Thr	Leu	Arg	Gln	Cys	Ile	Glu	Val	Leu	Arg	Arg	Asn	Gln	Lys	Ser
		355					360					365			
Ser	Ser	Gln	Asn	Leu	Glu	Gln	Val	Pro	Tyr	Arg	Gln	Ser	Lys	Leu	Thr
		370				375					380				
His	Leu	Phe	Lys	Asn	Tyr	Leu	Glu	Gly	Asn	Gly	Lys	Ile	Arg	Met	Val
385				390						395					400

Ile Cys Val Asn Pro Lys Pro Asp Asp Tyr Asp Glu Asn Met Ser Ala  
 405 410 415

Leu Ala Phe Ala Glu Glu Ser Gln Thr Ile Glu Val Lys Lys Gln Val  
 420 425 430

Glu Arg Met Pro Ser Glu Arg Ile Pro His Ser Phe Phe Thr Gln Trp  
 435 440 445

Asn Ser Glu Leu Asp Gly Ser Val Arg Met Glu Asp Asp Gly Ser Arg  
 450 455 460

Glu Ile Pro Cys Pro Pro Thr Phe Cys Leu Thr Asp Cys Asn Asp Lys  
 465 470 475 480

Asp Thr Val Asp Ser Met Tyr Lys Tyr Ala Arg Lys Leu Ser Ser Leu  
 485 490 495

Gln Asn Ser Ser Glu Glu Gly Pro Ser Ser Thr Leu Leu Thr Met Ile  
 500 505 510

Arg Gln Tyr Met Met Glu Ala Asp Tyr Gln Arg Val Glu Ile Ala Arg  
 515 520 525

Leu Lys Asp Ser Leu Asn Asp Lys Asp Glu Glu Ile Lys Lys Leu Arg  
 530 535 540

Gly Phe Cys Ser Arg Tyr Lys Arg Glu Asn Ala Ser Met Lys Glu Arg  
 545 550 555 560

Ile Ala Ser Cys Glu Gln Gly Glu Gln Glu Asn Ala Leu Val Met Glu  
 565 570 575

Lys Leu Met Glu Gln Lys Met Glu Asp Arg Lys Ile Ile Gln Ser Gln  
 580 585 590

Lys Lys Ala Met Arg Asn Val Arg Gly Ile Ile Asp Asn Pro Ser Pro  
 595 600 605

Ser Val Ala Ser Leu Arg Ser Arg Phe Asp Gln Glu Asn Val Ala His  
 610 615 620

Pro Thr Ala Pro Ile Gln Thr Pro Pro Pro Pro Tyr Gln Thr Pro Gly  
 625 630 635 640

Arg Ala Pro Val Phe Lys Lys Arg Leu Glu Ala Thr Thr Ser Thr Thr  
645 650 655

Val Met Ser Gly Ser Ser Ser Gly Gly Ser Gly Gln Gln Gly Tyr Val  
660 665 670

Asn Pro Lys Tyr Gln Arg Arg Ser Lys Ser Ala Ser Arg Leu Leu Asp  
675 680 685

His Gln Pro Leu His Arg Val Pro Thr Gly Thr Val Leu Gln Ser Arg  
690 695 700

Thr Pro Ala Asn Ala Ile Arg Thr Thr Lys Pro Glu Met His Gln Leu  
705 710 715 720

Asn Lys Ser Gly Glu Tyr Arg Leu Thr His Gln Glu Val Asp Asp Glu  
725 730 735

Gly Asn Ile Ser Thr Asn Ile Val Lys Val Asn Ser Leu Val Ser Thr  
740 745 750

Gln Lys His Ala Cys Thr Val Pro Leu Ser Phe Ser Arg Val Leu Ile  
755 760 765

Thr His Leu Ser  
770

<210> 8  
<211> 856  
<212> PRT  
<213> Homo sapiens

<400> 8

Met Lys Ser Ala Arg Ala Lys Thr Pro Arg Lys Pro Thr Val Lys Lys  
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Gly Ser Gln Thr Asn Leu Lys Asp Pro Val Gly Val Tyr Cys Arg Val  
20 25 30

Arg Pro Leu Gly Phe Pro Asp Gln Glu Cys Cys Ile Glu Val Ile Asn  
35 40 45

Asn Thr Thr Val Gln Leu His Thr Pro Glu Gly Tyr Arg Leu Asn Arg  
50 55 60

Asn Gly Asp Tyr Lys Glu Thr Gln Tyr Ser Phe Lys Gln Val Phe Gly  
65 70 75 80

Thr His Thr Thr Gln Lys Glu Leu Phe Asp Val Val Ala Asn Pro Leu  
 85 90 95

Val Asn Asp Leu Ile His Gly Lys Asn Gly Leu Leu Phe Thr Tyr Gly  
 100 105 110

Val Thr Gly Ser Gly Lys Thr His Thr Met Thr Gly Ser Pro Gly Glu  
 115 120 125

Gly Gly Leu Leu Pro Arg Cys Leu Asp Met Ile Phe Asn Ser Ile Gly  
 130 135 140

Ser Phe Gln Ala Lys Arg Tyr Val Phe Lys Ser Asn Asp Arg Asn Ser  
 145 150 155 160

Met Asp Ile Gln Cys Glu Val Asp Ala Leu Leu Glu Arg Gln Lys Arg  
 165 170 175

Glu Ala Met Pro Asn Pro Lys Thr Ser Ser Ser Lys Arg Gln Val Asp  
 180 185 190

Pro Glu Phe Ala Asp Met Ile Thr Val Gln Glu Phe Cys Lys Ala Glu  
 195 200 205

Glu Val Asp Glu Asp Ser Val Tyr Gly Val Phe Val Ser Tyr Ile Glu  
 210 215 220

Ile Tyr Asn Asn Tyr Ile Tyr Asp Leu Leu Glu Glu Val Pro Phe Asp  
 225 230 235 240

Pro Ile Lys Pro Lys Pro Pro Gln Ser Lys Leu Leu Arg Glu Asp Lys  
 245 250 255

Asn His Asn Met Tyr Val Ala Gly Cys Thr Glu Val Glu Val Lys Ser  
 260 265 270

Thr Glu Glu Ala Phe Glu Val Phe Trp Arg Gly Gln Lys Lys Arg Arg  
 275 280 285

Ile Ala Asn Thr His Leu Asn Arg Glu Ser Ser Arg Ser His Ser Val  
 290 295 300

Phe Asn Ile Lys Leu Val Gln Ala Pro Leu Asp Ala Asp Gly Asp Asn  
 305 310 315 320

Val Leu Gln Glu Lys Glu Gln Ile Thr Ile Ser Gln Leu Ser Leu Val  
 325 330 335

Asp Leu Ala Gly Ser Glu Arg Thr Asn Arg Thr Arg Ala Glu Gly Asn  
 340 345 350

Arg Leu Arg Glu Ala Gly Asn Ile Asn Gln Ser Leu Met Thr Leu Arg  
 355 360 365

Thr Cys Met Asp Val Leu Arg Glu Asn Gln Met Tyr Gly Thr Asn Lys  
 370 375 380

Met Val Pro Tyr Arg Asp Ser Lys Leu Thr His Leu Phe Lys Asn Tyr  
 385 390 395 400

Phe Asp Gly Glu Gly Lys Val Arg Met Ile Val Cys Val Asn Pro Lys  
 405 410 415

Ala Glu Asp Tyr Glu Glu Asn Leu Gln Val Met Arg Phe Ala Glu Val  
 420 425 430

Thr Gln Glu Val Glu Val Ala Arg Pro Val Asp Lys Ala Ile Cys Gly  
 435 440 445

Leu Thr Pro Gly Arg Arg Tyr Arg Asn Gln Pro Arg Gly Pro Val Gly  
 450 455 460

Asn Glu Pro Leu Val Thr Asp Val Val Leu Gln Ser Phe Pro Pro Leu  
 465 470 475 480

Pro Ser Cys Glu Ile Leu Asp Ile Asn Asp Glu Gln Thr Leu Pro Arg  
 485 490 495

Leu Ile Glu Ala Leu Glu Lys Arg His Asn Leu Arg Gln Met Met Ile  
 500 505 510

Asp Glu Phe Asn Lys Gln Ser Asn Ala Phe Lys Ala Leu Leu Gln Glu  
 515 520 525

Phe Asp Asn Ala Val Leu Ser Lys Glu Asn His Met Gln Gly Lys Leu  
 530 535 540

Asn Glu Lys Glu Lys Met Ile Ser Gly Gln Lys Leu Glu Ile Glu Arg  
 545 550 555 560

Leu Glu Lys Lys Asn Lys Thr Leu Glu Tyr Lys Ile Glu Ile Leu Glu  
565 570 575

Lys Thr Thr Thr Ile Tyr Glu Glu Asp Lys Arg Asn Leu Gln Gln Glu  
580 585 590

Leu Glu Thr Gln Asn Gln Lys Leu Gln Arg Gln Phe Ser Asp Lys Arg  
595 600 605

Arg Leu Glu Ala Arg Leu Gln Gly Met Val Thr Glu Thr Thr Met Lys  
610 615 620

Trp Glu Lys Glu Cys Glu Arg Arg Val Ala Ala Lys Gln Leu Glu Met  
625 630 635 640

Gln Asn Lys Leu Trp Val Lys Asp Glu Lys Leu Lys Gln Leu Lys Ala  
645 650 655

Ile Val Thr Glu Pro Lys Thr Glu Lys Pro Glu Arg Pro Ser Arg Glu  
660 665 670

Arg Asp Arg Glu Lys Val Thr Gln Arg Ser Val Ser Pro Ser Pro Val  
675 680 685

Pro Leu Leu Phe Gln Pro Asp Gln Asn Ala Pro Pro Ile Arg Leu Arg  
690 695 700

His Arg Arg Ser Arg Ser Ala Gly Asp Arg Trp Val Asp His Lys Pro  
705 710 715 720

Ala Ser Asn Met Gln Thr Glu Thr Val Met Gln Pro His Val Pro His  
725 730 735

Ala Ile Thr Val Ser Val Ala Asn Glu Lys Ala Leu Ala Lys Cys Glu  
740 745 750

Lys Tyr Met Leu Thr His Gln Glu Leu Ala Ser Asp Gly Glu Ile Glu  
755 760 765

Thr Lys Leu Ile Lys Gly Asp Ile Tyr Lys Thr Arg Gly Gly Gly Gln  
770 775 780

Ser Val Gln Phe Thr Asp Ile Glu Thr Leu Lys Gln Glu Ser Pro Asn  
785 790 795 800

Gly Ser Arg Lys Arg Arg Ser Ser Thr Val Ala Pro Ala Gln Pro Asp



805

810

815

Gly Ala Glu Ser Glu Trp Thr Asp Val Glu Thr Arg Cys Ser Val Ala  
820 825 830

Val Glu Met Arg Ala Gly Ser Gln Leu Gly Pro Gly Tyr Gln His His  
835 840 845

Ala Gln Pro Lys Arg Lys Lys Pro  
850 855